

## SEQUENCE LISTING

<110> Ross et al.

<120> Polypeptides Containing Glycosylphosphatidyinositol

<130> 71838-01

<150> PCT/GB04/001572

<151> 2004-04-07

<150> 032435.1

<151> 2003-10-16

<150> 0308088.4

<151> 2003-04-09

<160> 20

<170> PatentIn version 3.1

<210> 1

<211> 794

<212> DNA

<213> Artificial sequence

<220>

<223> fusion protein comprising growth hormone fused to domain comprising glycosylphosphatidyinositol

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Asp Ala His Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn  
20 25 30

Ala Ser Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr  
35 40 45

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe  
50 55 60

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr  
65 70 75 80

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu  
85 90 95

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe  
100 105 110

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser  
115 120 125

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu  
130 135 140

Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys  
145 150 155 160

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu  
165 170 175

Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys  
180 185 190

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser  
195 200 205

Cys Gly Phe Gly Gly Gly Gly Asp Ile Asp Lys Leu Val Lys Cys Gly  
210 215 220

Gly Ile Ser Leu Leu Val Gln Asn Thr Ser Trp Met Leu Leu Leu Leu  
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Leu Ser Leu Ser Leu Leu Gln Ala Leu Asp Phe Ile Ser Leu  
245 250

<210> 3  
<211> 1607  
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<223> fusion protein comprising growth hormone fused to growth hormone  
receptor

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gcagcccccg gactgggcag atcttcaagc agacctacag caagttcgac acaaactcac 540  
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tgggtcaagtg tggcggcata agcctgctgg ttcagaacac atcctggatg ctgctgctgc     1560
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<211> 525

<212> PRT

<213> Artificial Sequence

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<223> fusion protein comprising growth hormone fused to growth hormone  
receptor

<400> 4

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Asp Ala His Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn
          20           25           30

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Ala Ser Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr
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Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe
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Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr

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Arg	Ile	Ser	Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe
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Thr Arg Arg Asn Thr Gln Glu Trp Thr Gln Glu Trp Lys Glu Cys Pro  
 305 310 315 320

Asp Tyr Val Ser Ala Gly Glu Asn Ser Cys Tyr Phe Asn Ser Ser Phe  
 325 330 335

Thr Ser Ile Trp Ile Pro Tyr Cys Ile Lys Leu Thr Ser Asn Gly Gly  
 340 345 350

Thr Val Asp Glu Lys Cys Phe Ser Val Asp Glu Ile Val Gln Pro Asp  
 355 360 365

Pro Pro Ile Ala Leu Asn Trp Thr Leu Leu Asn Val Ser Leu Thr Gly  
 370 375 380

Ile His Ala Asp Ile Gln Val Arg Trp Glu Ala Pro Arg Asn Ala Asp  
 385 390 395 400

Ile Gln Lys Gly Trp Met Val Leu Glu Tyr Glu Leu Gln Tyr Lys Glu  
 405 410 415

Val Asn Glu Thr Lys Trp Lys Met Met Asp Pro Ile Leu Thr Thr Ser  
 420 425 430

Val Pro Val Tyr Ser Leu Lys Val Asp Lys Glu Tyr Glu Val Arg Val  
 435 440 445

Arg Ser Lys Gln Arg Asn Ser Gly Asn Tyr Gly Glu Phe Ser Glu Val  
 450 455 460

Leu Tyr Val Thr Leu Pro Gln Met Ser Gln Phe Thr Cys Glu Glu Asp  
 465 470 475 480

Phe Tyr Gly Gly Gly Gly Asp Ile Asp Lys Leu Val Lys Cys Gly Gly  
 485 490 495

Ile Ser Leu Leu Val Gln Asn Thr Ser Trp Met Leu Leu Leu Leu Leu  
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 ttgaagaagc ctatatccca aaggaacaga agtattcatt cctgcagaac cccagacct 240  
 ccctctgttt ctgagagtct attccgacac cctccaacag ggaggaaaca caacagaaat 300  
 ccaacctaga gctgctccgc atctccctgc tgctcatcca gtcgtggctg gagcccgtgc 360  
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 acaaggtcga gacattcctg cgcacgtgc agtgccgctc tgtggagggc agctgtggct 660  
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 cattcctgcg catcgtgcag tgccgctctg tggagggcag ctgtggcttc ggcggtggag 1320  
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1442

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Ala Ser Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr  
35 40 45

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe  
50 55 60

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr  
65 70 75 80

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu  
85 90 95

Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe  
100 105 110

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser  
115 120 125

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu  
130 135 140

Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys  
145 150 155 160

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu  
165 170 175



Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys  
180 185 190

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser  
195 200 205

Cys Gly Phe Gly Gly Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
210 215 220

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Phe Phe Pro Thr Ile  
225 230 235 240

Pro Leu Ser Arg Leu Phe Asp Asn Ala Ser Leu Arg Ala His Arg Leu  
245 250 255

His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile  
260 265 270

Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu  
275 280 285

Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln  
290 295 300

Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln  
305 310 315 320

Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser  
325 330 335

Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp  
340 345 350

Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser  
355 360 365

Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr  
370 375 380

Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr  
385 390 395 400

Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val  
405 410 415

Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Gly Gly Gly Gly Asp  
420 425 430

Ile Asp Lys Leu Val Lys Cys Gly Gly Ile Ser Leu Leu Val Gln Asn  
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<210> 9  
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<212> DNA  
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<210> 11  
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Leu Ile  
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<220>  
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receptor

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<400> 17

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<400> 18

Pro Gly Ile Ser Gly Gly Gly Gly Gly Gly  
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<210> 19  
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<400> 19

Leu Val Pro Arg Gly Ser Pro Gly Ile Ser Gly Gly Gly Gly Gly Gly  
1 5 10 15

<210> 20  
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<220>  
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<400> 20

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